SEQUENCE LISTING

<110> ALDAZ, MARCELO C.
      BEDNAREK, ANDRZEJ

<120> WWOX: A PUTATIVE TUMOR SUPPRESSOR GENE MUTATED IN
      MULTIPLE CANCERS

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<140> UNKNOWN
<141> 2001-10-15

<150> 60/240,277
<151> 2000-10-13

<160> 68

<170> PatentIn Ver. 2.1

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gac ggc tgg gtt tac tac gcc aat cac acc gag gag aag act cag tgg   265
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tac gga tgg gaa caa gaa act gat gag aac gga caa gtg ttt ttt gtt   361
Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val
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gac cat ata aat aaa aga acc acc tac ttg gac cca aga ctg gcg ttt   409
Asp His Ile Asn Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe
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Gly Trp Ala His Thr Pro Ala Leu Cys Val Ser Pro His Ala Ser Ala
205             210             215             220

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Arg Ala Gly Pro Leu Pro Asn Val Pro Pro Thr Gln Ile Arg Lys Ser
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aaa gga aat aag agc agt cac aac aga gtg aaa aat ctt aag tac caa    889
Lys Gly Asn Lys Ser Ser His Asn Arg Val Lys Asn Leu Lys Tyr Gln
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gct agg cat agg tct ctt tgc ttt ctg gtg gtg gcc tgt ttg aaa gta    985
Ala Arg His Arg Ser Leu Cys Phe Leu Val Val Ala Cys Leu Lys Val
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caa ttc tct ttc ttt tac tgt tat aga ata gcc tga ggtcccctcg    1079
Gln Phe Ser Phe Phe Tyr Cys Tyr Arg Ile Ala
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         30                  35                  40

gaa cat cca aaa act gga aaa aga aaa cga gtg gca gga gat ttg cca   313
Glu His Pro Lys Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro
 45                  50                  55                  60

tac gga tgg gaa caa gaa act gat gag aac gga caa gtg ttt ttt gtt   361
Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val
                 65                  70                  75

gac cat ata aat aaa aga acc acc tac ttg gac cca aga ctg gcg ttt   409
Asp His Ile Asn Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe
                 80                  85                  90

act gtg gat gat aat ccg acc aag cca acc acc cgg caa aga tac gac   457
Thr Val Asp Asp Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp
             95                  100                 105

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Gly Ser Thr Thr Ala Met Glu Ile Leu Gln Gly Arg Asp Phe Thr Gly
         110                 115                 120

aaa gtg gtt gtg gtc act gga gct aat tca gga ata ggg ttc gaa acc   553
Lys Val Val Val Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr
125                 130                 135                 140

gcc aag tct ttt gcc ctc cat ggt gca cat gtg atc ttg gcc tgc agg   601
Ala Lys Ser Phe Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg
                 145                 150                 155

aac atg gca agg gcg agt gaa gca gtg tca cgc att tta gaa gaa tgg   649
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12

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Asn Met Ala Arg Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp
            160                 165                 170

caa cag gga gct gcc acc acc gtg tac tgt gct gct gtc cca gaa ctg    697
Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu
            175                 180                 185

gag ggt ctg gga ggg atg tac ttc aac aac tgc tgc cgc tgc atg ccc    745
Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro
        190                 195                 200

tca cca gaa gct cag agc gaa gag acg gcc cgg acc ctg tgg gcg ctc    793
Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu
205                 210                 215                 220

agc gag agg ctg atc caa gaa cgg ctt ggc agc cag tcc ggc taa        838
Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
                225                 230                 235

gtggagctca gagcggatgg gcacacacac ccgccctgtg tgtgtcccct cacgcaagtg  898

ccagggctgg gccccttcca aatgtccctc caacacagat ccgcaagagt aaaggaaata  958

agagcagtca caacagagtg aaaaatctta agtaccaatg ggaagcaggg aattcctggg  1018

gtaaagtatc acttttctgg ggctgggcta ggcataggtc tctttgcttt ctggtggtgg  1078

cctgtttgaa agtaaaaacc tgcttggtgt gtaggttccg tatctccctg gagaagcacc  1138

agcaattctc tttcttttac tgttatagaa tagcctgagg tcccctcgtc ccatccagct  1198

accaccacgg ccaccactgc agccgggggc tggccttctc ctacttaggg aagaaaaagc  1258

aagtgttcac tgctccttgc tgcattgatc caggagataa ttgtttcatt catcctgacc  1318

aagactgagc cagcttagca actgctgggg agacaaatct cagaaccttg tcccagccag  1378

tgaggatgac agtgacaccc agagggagta gaatacgcag aactaccagg tggcaaagta  1438

cttgtcatag actcctttgc taatgctatg caaaaaattc tttagagatt ataacaaatt  1498

tttcaaatca ttccttagat accttgaaag gcaggaaggg aagcgtatat acttaagaat  1558

acacaggata ttttgggggg cagagaataa aacgttagtt aatccctttg tctgtcaatc  1618

acagtctcag ttctcttgct ttcacattgt acttaaacct cctgctgtgc ctcgcatcct  1678

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13

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            20                  25                  30
Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys
            35                  40                  45
Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
        50                  55                  60
Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
65                  70                  75                      80
Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
                85                  90                  95
Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
            100                 105                 110
Ala Met Glu Ile Leu Gln Gly Arg Asp Phe Thr Gly Lys Val Val Val
        115                 120                 125
Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
    130                 135                 140
Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg
145                 150                 155                 160
Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp Gln Gln Gly Ala
            165                 170                 175
Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu Glu Gly Leu Gly
        180                 185                 190
Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro Ser Pro Glu Ala
        195                 200                 205
Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu Ser Glu Arg Leu
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Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
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